Appendix S1. Rapid eradication assessment for ship rats following Brook Waimārama Sanctuary eradication attempt.

To test the eradication assumption we use the rapid eradication assessment tool REA shiny, <u>https://rea.docker.stat.auckland.ac.nz/</u> (Kim et al. 2020). The inputs are provided in Supplementary Materials. All varying parameters described below are input as PERT distributions for Monte Carlo draws in the Bayesian calculation and are quoted as *mode* [*minimum*, *maximum*].

Rat home ranges are assumed to be bivariate normal with 1-D standard deviation parameter σ = 20 m, corresponding to 95% occupancy area of 0.75 ha (Samaniego-Herrera et al. 2013; Nathan 2016). There are no published values for rats at the limit of low density but it is expected that home range will only increase at lower densities, making rats more detectable over long time periods, so that these values are conservative. The range of σ is set to [15,26] m (Kim et al. 2020). Detecting devices are the 2041 tracking tunnels and 306 DOC 200 traps. Detection probability parameter g_0 (Samaniego-Herrera et al. 2013) is estimated to be 0.05 [0.03, 0.09] per night for tracking tunnels and 0.10 [0.05, 0.15] per night for DOC 200 traps. We use 0.5 [0.1, 0.9] as a relatively uninformative Bayesian prior probability of eradication.

The result is a posterior distribution with over 97.5% of Monte Carlo draws above 53% certain that eradication was successful. The median was over 95% certain. Intuitively this is as expected – over 2000 devices approximately evenly spaced in 690 ha means a least one, and often multiple, devices per 0.5 –1.0 ha home range, and 180 nights is many times $1/g_0$, so that animals should be detected.

References

- Kim JHK, Corson P, Mulgan N, Russell JC 2020. Rapid eradication assessment (REA): A tool for pest absence confirmation. Wildlife Research 47(2): 128–136.
- Nathan HW 2016. Detection probability of invasive ship rats: biological causation and management

implications. Unpublished PhD thesis. University of Auckland, Auckland, New Zealand.

Samaniego-Herrera A, Anderson DP, Parkes JP, Aguirre-Muñoz A 2013. Rapid assessment of rat eradication after aerial baiting. Journal of Applied Ecology 50(6): 1415–1421.

Appendix S2. Brook Waimārama Sanctuary surveillance network.

Map shows the surveillance network within Brook Waimarama Sanctuary during the period from April 2018 – January 2020 showing locations of permanent devices targeting rodents.



Appendix S3. Frequency of number of loci consistent with the mother.

An exact calculation of the probability of one rat having a genotype consistent with being the offspring of another is not possible without knowledge of the distribution of alleles in the population, but an approximation can be derived as follows.

The frequency of number of loci consistent with the mother is shown in the table below.

Number of loci, out	Number of					
of nine, consistent	Individuals					
with mother						
0	0					
1	0					
2	0					
3	0					
4	2					
5	2					
6	0					
7	0					
8	0					
9	12					
Total	16					

The simplest explanation for this bimodal distribution is that 12 are offspring of the mother, 4 are not, and the probability of a locus being consistent with the mother by chance is 2x4 + 2x5 = 18 out of 4x9 = 36, giving a maximum likelihood probability of locus match of p = 0.5. The assumptions here are Hardy-Wineburg equilibrium, that all loci are independent, and that the probability of a random match is independent of the locus, so that a binomial distribution is appropriate. (In practice the probability will vary with the locus, the mother's alleles, and her homo- or hetero-zygosity, but this approximation is reasonable for the order of magnitude calculation that follows.) The probability of 18 out of 36 matches is then $P_0 = Bin(18, 36, 0.5) = 0.13$, where Bin(x, n, p) is the binomial distribution for x successes out of n trials with trial probability p.

The counterfactual is that one of the 12 complete (9 out of 9 loci) matches occurred by chance. The probability of a locus match with the mother would then be 27 out of 45 giving a maximum likelihood p = 0.6. Then the probability of 18 out of 36 matches together with 9 out of 9 is $P_1 = Bin(18, 36, 0.6) \times Bin(9, 9, 0.6) = 0.00064$. The ratio P_1/P_0 is then 0.5%, which gives a measure of the likelihood of the counterfactual - almost certainly not the case.

Appendix S4: Genetic profiles of all genotyped rats and inference on relatedness.

The table overleaf shows the genetic profiles of all available rat carcasses, showing alleles at nine microsatellite loci (genotyping by Ecogene Ltd). The top row shows the profile of the putative mother. Bold text indicates loci with private alleles (i.e. no match to mother), indicating that the individual cannot be the offspring of the mother. Twelve individuals remain as probable offspring. Partial genetic profiles of at least two fathers are inferred. Italicised and underlined text indicates an individual that cannot be the offspring of Inferred Father 1 due to private alleles. The inferred genotype of Father 1 is based on him being the father of all individuals not ruled out, i.e., BWSnn where nn = 03 - 07, 09 - 13, 15. The genotype of Father 2 is based on him being the father of BWS16. Other combinations of two or more fathers are possible.

The only male of the four non-offspring is BWS02. He cannot be the father of any of the twelve probable offspring as his D18 and D20 alleles do not match any of the twelve.

Similarly, if the female had mated with one of her offspring, the only candidates, by weight as a proxy for maturity, and sex, are BWS11 and BWS15. BWS11 is ruled out as father of all eleven remaining by a combination of D18, D5, D7 and D11. BWS15 is ruled out as father of nine of the eleven remaining by D15, D18, D7 and D11. We therefore conclude that the father of most of the rats was almost certainly not captured.

All available genetic profiles with inference on relatedness.

Rat ID	Sex	D1	10		015	D	16		D18	D	20	D	2	D	5	D7		D11		Loci consistent with Mother
Mother	F	128	128	217	236	165	165	209	211	149	149	97	105	172	172	154	182	222	272	
BWS02	м	96	128	236	236	165	165	240	242	147	177	105	105	172	172	184	188	276	276	5
BWS03	F	96	128	236	238+	165	165	211	238	149	149	105	105	164 ^	172	154	184 ^	272	₂₇₈ †^	9
BWS04	F	96	128	217	236	165	165	211	238	149	149	97	105	172	172	180†	182	222	278*^	9
BWS05	F	96	128	236	238+	165	165	211	₂₄₄ †^	149	149	105	105	164 ^	172	180†	182	222	278*^	9
BWS06	F	128	128	217	236	165	165	211	₂₄₄ †^	149	149	97	105	172	172	182	184 ^	222	280	9
BWS07	*	128	128	236	238+	165	165	209	238	149	181	97	105	164 ^	172	154	180+	222	280	9
BWS08	F	96	96	217	217	165	165	238	242	181	181	105	111	170	170	184	188	272	280	4
BWS09	F	128	128	236	236	165	165	209	238	149	149	105	105	164 ^	172	182	184 ^	272	280	9
BWS10	F	128	128	236	238+	165	165	209	₂₄₄ †^	149	149	97	105	164 ^	172	154	180+	222	278*^	9
BWS11	м	96	128	236	238+	165	165	211	238	149	181	97	105	172	172	154	180+	272	280	9
BWS12	F	128	128	236	236	165	165	209	₂₄₄ †^	149	149	105	105	172	172	180†	182	272	280	9
BWS13	м	128	128	236	238+	165	165	209	₂₄₄ †^	149	181	97	105	172	172	180†	182	272	280	9
BWS14	F	128	128	236	242	165	165	213	242	149	177	105	127	170	170	184	190	278	278	5
BWS15	М	96	128	236	236	165	165	209	238	149	181	97	105	164 ^	172	182	184 ^	222	280	9
BWS16	М	128	128	236	236	165	165	211	238	149	149	97	105	172	172	<u>182</u>	<u>182</u>	<u>272</u>	<u>272</u> †	<u>9</u>
BWS18	F	96	96	234	238	165	165	240	242	181	181	105	127	170	172	182	188	278	278	4
Inferred F	ather 1	96	128	236	238	165	165	238	244	149	181	105	?	164	172	180	184	278	280	
Inferred F	ather 2	128	?	236	?	165	?	238	?	149	?	97 or 105	?	172	?	182	?	272	?	

Bold text indicates loci with private alleles (i.e. no match to mother), indicating that the individual cannot be the offspring of the mother.

Italicised and underlined text indicates an individual that cannot be the offspring of Inferred Father 1 due to private alleles

*Indeterminate sex – genetic and phenotypic sex assignments in disagreement

⁺ This allele rules out being offspring of mother and BWS15

^ This allele rules out being offspring of mother and BWS11

Appendix S5. Head-body length (mm) and weight (g) of probable offspring and distance to mother's location.

The figure below shows the head-body length (mm) and weight (g) of probable offspring plotted against the distance between their recovery locations and that of the mother. The two graphs appear very similar, because of the strong correlation between length and weight of growing rats.

In addition to the linear models reported in the main paper, we also tested for log(response) and exponential relationships. After removing the outlier data point for the male that moved 1510 m neither probable offspring weight nor head-body length was significantly related to the distance between the mother and probable offspring's recovery locations (see table below).



Head-body length (mm) and weight (g) of probable offspring and distance to mother's location.

Results of alternative models for relationships between distance between the mother and probable offspring's recovery locations and weight, or head-body length (HBL).

Model	r ²	F (1,9)	р
Distance to mother ~ log(weight)	0.09	2.0	0.19
log(Distance to mother)~ weight	0.06	0.5	0.51
Distance to mother ~ log(HBL)	0.14	2.6	0.19
log(Distance to mother)~ HBL	-0.04	0.6	0.46